1652

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/707,121

DATE: 06/22/2001
TIME: 14:31:35

Input Set : A:\LEX-0083-USA.SEQLIST.txt
Output Set: N:\CRF3\06222001\I707121.raw

ENTERED

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   4 <110> APPLICANT: Mathur, Brian
   5       Turner, C. Alexander Jr.
   6       Abuin, Alejandro
   7       Friedrich, Glenn
   8       Zambrowicz, Brian
   9       Sands, Arthur T.
  11 <120> TITLE OF INVENTION: Novel Human Kinase Protein and
  12       Polynucleotides Encoding the Same
  15 <130> FILE REFERENCE: LEX-0083-USA
C--> 17 <140> CURRENT APPLICATION NUMBER: US/09/707,121
C--> 17 <141> CURRENT FILING DATE: 2000-11-06
  17 <150> PRIOR APPLICATION NUMBER: US 60/164,289
  18 <151> PRIOR FILING DATE: 1999-11-08
  20 <160> NUMBER OF SEQ ID NOS: 2
  22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
  24 <210> SEQ ID NO: 1
  25 <211> LENGTH: 2682
  26 <212> TYPE: DNA
  27 <213> ORGANISM: homo sapiens
  29 <400> SEQUENCE: 1
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  31 catgatgttt gtggaagcaa tggacttcct ctcacaccaa attccatcaa aattttaggg     120
  32 cgctttcaaa tccttaaaac catcacccat cccagactct gccagtatgt ggatatttct     180
  33 aggggaaagc atgaacgact agtggtcgtg gctgaacatt gtgaacgtag tctggaagac     240
  34 ttgcttcgag aaaggaaacc tgtgagctgt tcaacggttt tgtgtatagc atttgaggtt     300
  35 cttcagggct tgcagtatat gaacaaacat ggtatagtac acagggcatt gtctcctcat     360
  36 aatatcctgt tggaccgaaa gggacatatt aaattggcta aatttggact ttatcacatg     420
  37 acagctcatg gtgatgatgt tgatttccca atagggtatc cctcgtactt ggcccctgag     480
  38 gtaattgcac agggaatttt caaaaccact gatcacatgc caagtaaaaa accattgcct     540
  39 tctggcccca aatcagatgt atggtctctt ggaatcattt tatttgagct ttgtgtggga     600
  40 agaaaattat ttcagagctt ggatatttct gaaagactaa aatttttgct tactttggat     660
  41 tgtgtagatg acactttaat agttctggct gaagagcatg gttgtttgga cattataaag     720
  42 gagcttcctg aaactgtgat agatcttttg aataagtgcc ttaccttcca tccttctaag     780
  43 aggccaaccc cagatgaatt aatgaaggac aaagtattca gtgaggtatc acctttatat     840
  44 acccccttta ccaaacctgc cagtctgttt tcatcttctc tgagatgtgc tgatttaact     900
  45 ctgcctgagg atatcagtca gttgtgtaaa gatataaata atgattacct ggcagaaaga     960
  46 tctattgaag aagtgtatta cctttggtgt ttggctggag gtgacttgga gaaagagctt    1020
  47 gtcaacaagg aaatcattcg atccaaacca cctatctgca cactccccaa ttttctcttt    1080
  48 gaggatggtg aaagctttgg acaaggtcga gatagaagct cgcttttaga tgataccact    1140
  49 gtgacattgt cgttatgcca gctaagaaat agattgaaag atgttggtgg agaagcattt    1200
  50 tacccattac ttgaagatga ccagtctaat ttacctcatt caaacagcaa taatgagttg    1260
  51 tctgcagctg ccacgctccc tttaatcatc agagagaagg atacagagta ccaactaaat    1320
  52 agaattattc tcttcgacag gctgctaaag gcttatccat ataaaaaaaa ccaaatctgg    1380
  53 aaagaagcaa gagttgacat tcctcctctt atgagaggtt taacctgggc tgctcttctg    1440
  54 ggagttgagg gagctattca tgccaagtac gatgcaattg ataaagacac tccaattcct    1500
  55 acagatagac aaattgaagt ggatattcct cgctgtcatc agtacgatga actgttatca    1560
  56 tcaccagaag gtcatgcaaa atttaggcgt gtattaaaag cctgggtagt gtctcatcct    1620
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#5

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57 gatcttgtgt attggcaagg tcttgactca ctttgtgctc cattcctata tctaaacttc    1680
58 aataatgaag ccttggctta tgcatgtatg tctgctttta ttcccaaata cctgtataac    1740
59 ttcttcttaa aagacaactc acatgtaata caagagtatc tgactgtctt ctctcagatg    1800
60 attgcatttc atgatccaga gctgagtaat catctcaatg agattggttt cattccagat    1860
61 ctctatgcca tcccttggtt tcttaccatg tttactcatg tatttccact acacaaaatt    1920
62 ttccacctct gggatacctt actacttggg aattcctctt tcccattctg tattggagta    1980
63 gcaattcttc agcagctgcg ggaccggctt ttggctaatg gctttaatga gtgtattctt    2040
64 ctcttctccg atttaccaga aattgacatt gaacgctgtg tgagagaatc tatcaacctg    2100
65 ttttgttgga ctcctaaaag tgctacttac agacagcatg ctcaacctcc aaagccatct    2160
66 tctgacagca gtggaggcag aagttcggca ccttatttct ctgctgagtg tccagatcct    2220
67 ccaaagacag atctgtcaag agaatccatc ccattaaatg acctgaagtc agaagtatca    2280
68 ccacggattt cagcagagga cctgattgac ttgtgtgagc tcacagtgac aggccacttc    2340
69 aaaacaccca gcaagaaaac aaagtccagt aaaccaaagc tcctggtggt tgacatccgg    2400
70 aatagtgaag actttattcg tggtcacatt tcaggaagca tcaacattcc attcagtgct    2460
71 gccttcactg cagaagggga gcttacccag ggcccttaca ctgctatgct ccagaacttc    2520
72 aaagggaagg tcattgtcat cgtggggcat gtggcaaaac acacagctga gtttgcagct    2580
73 caccttgtga agatgaaata tccaagaatc tgtattctag atggtggcat taataaaata    2640
74 aagccaacag gcctcctcac catcccatct cctcaaatat ga                      2682
76 <210> SEQ ID NO: 2
77 <211> LENGTH: 893
78 <212> TYPE: PRT
79 <213> ORGANISM: homo sapiens
81 <400> SEQUENCE: 2
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84 Ser Ala Leu Pro His Asp Val Cys Gly Ser Asn Gly Leu Pro Leu Thr
85             20                  25                  30
86 Pro Asn Ser Ile Lys Ile Leu Gly Arg Phe Gln Ile Leu Lys Thr Ile
87         35                  40                  45
88 Thr His Pro Arg Leu Cys Gln Tyr Val Asp Ile Ser Arg Gly Lys His
89     50                  55                  60
90 Glu Arg Leu Val Val Val Ala Glu His Cys Glu Arg Ser Leu Glu Asp
91 65                  70                  75                  80
92 Leu Leu Arg Glu Arg Lys Pro Val Ser Cys Ser Thr Val Leu Cys Ile
93                 85                  90                  95
94 Ala Phe Glu Val Leu Gln Gly Leu Gln Tyr Met Asn Lys His Gly Ile
95             100                 105                 110
96 Val His Arg Ala Leu Ser Pro His Asn Ile Leu Leu Asp Arg Lys Gly
97         115                 120                 125
98 His Ile Lys Leu Ala Lys Phe Gly Leu Tyr His Met Thr Ala His Gly
99     130                 135                 140
100 Asp Asp Val Asp Phe Pro Ile Gly Tyr Pro Ser Tyr Leu Ala Pro Glu
101 145                 150                 155                 160
102 Val Ile Ala Gln Gly Ile Phe Lys Thr Thr Asp His Met Pro Ser Lys
103                 165                 170                 175
104 Lys Pro Leu Pro Ser Gly Pro Lys Ser Asp Val Trp Ser Leu Gly Ile
105             180                 185                 190
106 Ile Leu Phe Glu Leu Cys Val Gly Arg Lys Leu Phe Gln Ser Leu Asp
107         195                 200                 205
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108 Ile Ser Glu Arg Leu Lys Phe Leu Leu Thr Leu Asp Cys Val Asp Asp
109     210                 215                 220
110 Thr Leu Ile Val Leu Ala Glu Glu His Gly Cys Leu Asp Ile Ile Lys
111 225                 230                 235                 240
112 Glu Leu Pro Glu Thr Val Ile Asp Leu Leu Asn Lys Cys Leu Thr Phe
113                 245                 250                 255
114 His Pro Ser Lys Arg Pro Thr Pro Asp Glu Leu Met Lys Asp Lys Val
115             260                 265                 270
116 Phe Ser Glu Val Ser Pro Leu Tyr Thr Pro Phe Thr Lys Pro Ala Ser
117         275                 280                 285
118 Leu Phe Ser Ser Ser Leu Arg Cys Ala Asp Leu Thr Leu Pro Glu Asp
119     290                 295                 300
120 Ile Ser Gln Leu Cys Lys Asp Ile Asn Asn Asp Tyr Leu Ala Glu Arg
121 305                 310                 315                 320
122 Ser Ile Glu Glu Val Tyr Tyr Leu Trp Cys Leu Ala Gly Gly Asp Leu
123                 325                 330                 335
124 Glu Lys Glu Leu Val Asn Lys Glu Ile Ile Arg Ser Lys Pro Pro Ile
125             340                 345                 350
126 Cys Thr Leu Pro Asn Phe Leu Phe Glu Asp Gly Glu Ser Phe Gly Gln
127         355                 360                 365
128 Gly Arg Asp Arg Ser Ser Leu Leu Asp Asp Thr Thr Val Thr Leu Ser
129     370                 375                 380
130 Leu Cys Gln Leu Arg Asn Arg Leu Lys Asp Val Gly Gly Glu Ala Phe
131 385                 390                 395                 400
132 Tyr Pro Leu Leu Glu Asp Asp Gln Ser Asn Leu Pro His Ser Asn Ser
133                 405                 410                 415
134 Asn Asn Glu Leu Ser Ala Ala Ala Thr Leu Pro Leu Ile Ile Arg Glu
135             420                 425                 430
136 Lys Asp Thr Glu Tyr Gln Leu Asn Arg Ile Ile Leu Phe Asp Arg Leu
137         435                 440                 445
138 Leu Lys Ala Tyr Pro Tyr Lys Lys Asn Gln Ile Trp Lys Glu Ala Arg
139     450                 455                 460
140 Val Asp Ile Pro Pro Leu Met Arg Gly Leu Thr Trp Ala Ala Leu Leu
141 465                 470                 475                 480
142 Gly Val Glu Gly Ala Ile His Ala Lys Tyr Asp Ala Ile Asp Lys Asp
143                 485                 490                 495
144 Thr Pro Ile Pro Thr Asp Arg Gln Ile Glu Val Asp Ile Pro Arg Cys
145             500                 505                 510
146 His Gln Tyr Asp Glu Leu Leu Ser Ser Pro Glu Gly His Ala Lys Phe
147         515                 520                 525
148 Arg Arg Val Leu Lys Ala Trp Val Val Ser His Pro Asp Leu Val Tyr
149     530                 535                 540
150 Trp Gln Gly Leu Asp Ser Leu Cys Ala Pro Phe Leu Tyr Leu Asn Phe
151 545                 550                 555                 560
152 Asn Asn Glu Ala Leu Ala Tyr Ala Cys Met Ser Ala Phe Ile Pro Lys
153                 565                 570                 575
154 Tyr Leu Tyr Asn Phe Phe Leu Lys Asp Asn Ser His Val Ile Gln Glu
155             580                 585                 590
156 Tyr Leu Thr Val Phe Ser Gln Met Ile Ala Phe His Asp Pro Glu Leu
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```
157          595                 600                 605
158 Ser Asn His Leu Asn Glu Ile Gly Phe Ile Pro Asp Leu Tyr Ala Ile
159      610                 615                 620
160 Pro Trp Phe Leu Thr Met Phe Thr His Val Phe Pro Leu His Lys Ile
161  625                 630                 635                 640
162 Phe His Leu Trp Asp Thr Leu Leu Leu Gly Asn Ser Ser Phe Pro Phe
163                  645                 650                 655
164 Cys Ile Gly Val Ala Ile Leu Gln Gln Leu Arg Asp Arg Leu Leu Ala
165              660                 665                 670
166 Asn Gly Phe Asn Glu Cys Ile Leu Leu Phe Ser Asp Leu Pro Glu Ile
167          675                 680                 685
168 Asp Ile Glu Arg Cys Val Arg Glu Ser Ile Asn Leu Phe Cys Trp Thr
169      690                 695                 700
170 Pro Lys Ser Ala Thr Tyr Arg Gln His Ala Gln Pro Pro Lys Pro Ser
171  705                 710                 715                 720
172 Ser Asp Ser Ser Gly Gly Arg Ser Ser Ala Pro Tyr Phe Ser Ala Glu
173                  725                 730                 735
174 Cys Pro Asp Pro Pro Lys Thr Asp Leu Ser Arg Glu Ser Ile Pro Leu
175              740                 745                 750
176 Asn Asp Leu Lys Ser Glu Val Ser Pro Arg Ile Ser Ala Glu Asp Leu
177          755                 760                 765
178 Ile Asp Leu Cys Glu Leu Thr Val Thr Gly His Phe Lys Thr Pro Ser
179      770                 775                 780
180 Lys Lys Thr Lys Ser Ser Lys Pro Lys Leu Leu Val Val Asp Ile Arg
181  785                 790                 795                 800
182 Asn Ser Glu Asp Phe Ile Arg Gly His Ile Ser Gly Ser Ile Asn Ile
183                  805                 810                 815
184 Pro Phe Ser Ala Ala Phe Thr Ala Glu Gly Glu Leu Thr Gln Gly Pro
185              820                 825                 830
186 Tyr Thr Ala Met Leu Gln Asn Phe Lys Gly Lys Val Ile Val Ile Val
187          835                 840                 845
188 Gly His Val Ala Lys His Thr Ala Glu Phe Ala Ala His Leu Val Lys
189      850                 855                 860
190 Met Lys Tyr Pro Arg Ile Cys Ile Leu Asp Gly Gly Ile Asn Lys Ile
191  865                 870                 875                 880
192 Lys Pro Thr Gly Leu Leu Thr Ile Pro Ser Pro Gln Ile
193                  885                 890
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VERIFICATION SUMMARY DATE: 06/22/2001
PATENT APPLICATION: **US/09/707,121** TIME: 14:31:36

Input Set : **A:\LEX-0083-USA.SEQLIST.txt**
Output Set: **N:\CRF3\06222001\I707121.raw**

L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date